Patent
0796/66513

REMARKS

Claims 3, 5, 10-15, 17-19, 21-23, and 25-27 have been amended to reduce the filing fee. Favorable action is respectfully requested.

Respectfully submitted,
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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS

Claims 3, 5, 10-15, 17-19, 21-23, and 25-27 have been amended as follows:

--3. (Amended) The method according to claim 1 [or 2], characterized in that said polymorphism leads to an increased or decreased activation of genes of the lipid metabolism, in particular of the cholesterol metabolism.--

--5. (Amended) The method of [any one of] claim[s] 1 [to 4], characterized in that the presence of a polymorphism is determined at nucleic acid level.--

--10. (Amended) The method of [any one of] claim[s] 1 [to 4], characterized in that the detection of the presence of a polymorphism is done at amino acid level.--

--11. (Amended) Method of [any one of] claim[s] 1 [to 9], characterized in that after taking blood or a tissue sample, respectively, and DNA extraction at least a fragment of a SREBP exon comprising a polymorphism is amplified using two oligonucleotide sequences wherein said polymorphism is characteristic for an increased or decreased activation of genes of the lipid metabolism, in particular cholesterol metabolism, and that the product of said amplification is subjected to a digestion with a suitable restriction enzyme or a denaturation and that the digestion products or denaturation products, respectively, are separated electrophoretically.--

--12. (Amended) The method of claim 10 [or 11], characterized in that said polymorphism is characteristic for an increased or decreased risk for hypercholesterolemia in humans.--

--13. (Amended) The method of claim 11 [or 12], characterized in that at least one of said oligonucleotide sequences is located in the intron region which is adjacent to the exon

where said polymorphism exists.--

--14. (Amended) The method of [any one of] claim[s] 11 [to 13], characterized in that said oligonucleotide sequences are selected from the following pairs or from sequences which hybridize to said pairs under stringent conditions:

S1.18cF (Seq. Id. No. 9):

5'-TTATTTATAATCTGGGTTTTGTGTC-3' and

S1.18cR (Seq. Id. No. 10):

5'-GGGAAGAGCTAAGTTAAAAGTTGTG-3' or

***Eco*R I.S1.18cF** (Seq. Io. No. 11):

5'- CGGAATTCTGAAATTATTTATAATCTGGGTTTTGTGTC -3' and

***Eco*R I.S1.18cR** (Seq. Id. No. 12):

5'-CGGAATTCATCGGGGAAGAGCTAAGTTAAAAGTTGTG-3' or

S2.10P.F (Seq. Id. No. 13):

5'-GCCAGTGACCATTAACACCTTTTGA-3' and

S2.10P.R. (Seq. Id. No. 14):

5'-TCGTCTTCAAAGCCTGCCTCAGTGGCTGGC-3' or

***Eco*RI S2.10F** (Seq. Id. No. 15):

5'-CGGAATTCGCCAGTGACCATTAACACCTTTTGA-3' and

***Eco*RI S2.10R** (Seq. Id. No. 16):

5'-CGGAATTCTGCAGCAAGCCAGTCATCAGCAGCT-3'

***Eco*RI S2.6F** (Seq. Id. No. 17):

5'-CGGAATTCTGGTCTCACTGTGTTTTCACTCATC-3'

***Eco*RI S2.6R** (Seq. Id. No. 18):

5'-CGGAATTCGCCAGGGCTGACAAGCCTTTTCTCA-3'.--

--15. (Amended) The method of [any one of] claim[s] 1 [to 14], characterized in that said polymorphism has been detected by amplification and analysis of a SREBP sequence of interest, comparison of the exon regions of said sequence of interest to the exon regions of the type of sequence of the corresponding SREBP which is most often found in a population and examination of the sequences with found differences for dysfunction.--

--17. (Amended) Use of a method of [any one of] claim[s] 1 [to 16] for the detection of an increased or reduced risk for hypercholesterolemia and/or Alzheimer's disease.--

--18. (Amended) Use of a method of [any one of] claim[s] 11 [to 16] for the detection of an increased or decreased risk for the occurrence of side effects associated with HIV therapy, in particular the therapy with protease inhibitors.--

--19. (Amended) Use of a method of [any one of] claim[s] 1 [to 16] for an increased or decreased mortality risk.--

--21. (Amended) DNA and/or RNA chip [of claim 20] that comprises at least one polymorphism in a SREBP, in particular in SREBP-1 and/or SREBP-2 characterized in that said polymorphism is a polymorphism in SREBP-1 and/or SREBP-2 as defined in claim[s] 3[, 4 6, 7, 8 and 9].

--22. (Amended) DNA and/or RNA chip of claim 20 [or 21] comprising said polymorphism in presence of other polymorphisms which are diagnostic for the risk assessment of hypercholesterolemia and/or Alzheimer's disease.--

--23. (Amended) Use of a polymorphism [as defined in one of claims 3, 4, 6, 7, 8 and 9] that leads to an increased or decreased activation of genes of the lipid metabolism, in particular of the cholesterol metabolism, or of a chip of [one of] claim[s] 20 [to 22] as marker for the determination of an increased or reduced risk for the outbreak of a disease.--

--25. (Amended) Use of a polymorphism [as defined in one of claims 3, 4, 6, 7, 8 and 9] that leads to an increased or decreased activation of genes of the lipid metabolism, in particular of the cholesterol metabolism, or a chip of [one of] claim[s] 20 [to 22] for the determination of an increased or reduced risk for the occurrence of side effects associated with HIV therapy, in particular the therapy with protease inhibitors.--

--26. (Amended) Use of a polymorphism [as defined in one of claims 3, 4, 6, 7, 8 and 9] that leads to an increased or decreased activation of genes of the lipid metabolism, in particular of the cholesterol metabolism, or a chip of [one of] claim[s] 20 [to 22] for the determination of a reduced mortality risk.--

--27. (Amended) Use of a polymorphism [as defined in one of claims 3, 4, 6, 7, 8 and 9] that leads to an increased or decreased activation of genes of the lipid metabolism, in particular of the cholesterol metabolism, or a chip of [one of] claim[s] 20 [to 22] for the evaluation of a method of treatment for a disease selected from the group [comprising] consisting of hypercholesterolemia, Alzheimer's disease and HIV or for drug screening.--